NCBI   results of BLAST

BLASTN 2.1.3 [Apr-11-2001]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 990123014-1507-5082

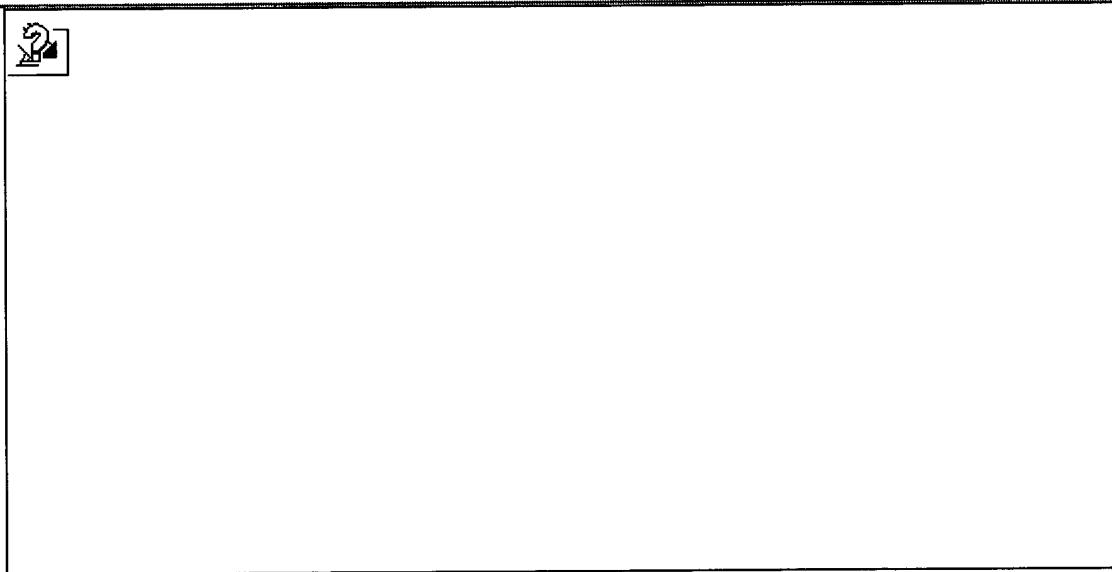**Query=**
        (2644 letters)

Database: nt
            861,799 sequences; 3,247,139,289 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 105 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

	Score (bits)	E Value
Sequences producing significant alignments:		
gi|13562129|gb|AY028435.1| Homo sapiens adaptor protein kan...	3478	0.0
gi|8922556|ref|NM_018158.1| Homo sapiens hypothetical prote...	3470	0.0
gi|7022771|dbj|AK001486.1|AK001486 Homo sapiens cDNA FLJ106...	3470	0.0
gi|13636382|ref|XM_002333.3| Homo sapiens hypothetical prot...	1949	0.0

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gi|2661089|gb|AF035526.1|AF035526    Mus musculus kanadaptin m...    1340    0.0
gi|1029496|emb|Z58265.1|HS33F3R      H.sapiens CpG island DNA ge...    428    e-117
gi|11182219|emb|AL357559.16|AL357559 Human DNA sequence fro...        141    2e-30
gi|11181843|gb|AC017028.11|AC017028  Homo sapiens BAC clone ...         48    0.028
gi|14010785|gb|AC069543.4|AC069543   Homo sapiens chromosome ...        46    0.11
gi|10443437|emb|AL356421.10|AL356421 Human DNA sequence fro...         46    0.11
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Alignments

>gi|13562129|gb|AY028435.1| Homo sapiens adaptor protein kanadaptin mRNA, complete cds
            Length = 2949

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 Score = 3478 bits (1754), Expect = 0.0
 Identities = 1758/1760 (99%)
 Strand = Plus / Plus


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Sbjct: 414   gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg 473


Query: 61    ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 474   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 533


Query: 121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 180
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Sbjct: 534   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 593


Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 240
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Sbjct: 594   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 653


Query: 241   ggaggagcagtcgcgcccacgacagcggtttcttcccctggcggtccagcccgggctcc 300
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Query: 301   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct 360
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Query: 361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg 420
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Sbjct: 774   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg 833


Query: 421   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 480
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Sbjct: 834   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 893


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Sbjct: 894   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta 953


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Query: 721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc 780
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Sbjct: 1194  agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga 1253


Query: 841   tgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 900
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Sbjct: 1254  tgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 1313


Query: 901   ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa 960
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Sbjct: 1314  ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa 1373


Query: 961   ggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1020
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Query: 1021  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca 1080
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Sbjct: 1494  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1553


Query: 1141  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa 1200
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Sbjct: 1854 tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt 1913


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Query: 1681 aggaggaagcaaattcaaattaaaaactggaacagtagggaagttacccccccaagcgtcc 1740
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 Strand = Plus / Plus


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>gi|8922556|ref|NM_018158.1| Homo sapiens hypothetical protein FLJ10624 (FLJ10624), mRNA
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Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 240
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Sbjct: 618   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 677

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Sbjct: 678   ggaggagcagtcgcgcccacgacagcggtttcttccctggcggtccagcccgggctcc 737

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct: 798   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgcctttcgg 857

Query: 421   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 480
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Query: 481   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta 540
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Query: 601   cacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctctt 660
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Query: 721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc 780
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Sbjct: 1218  agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga 1277

Query: 841   tgagatggggttgcacctgggggaatgggagaagatgcagtagaggatgatgctgaagagaa 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct: 1338  ccctattgtcttagagtttcagcaggaaagggaggcctttttatataaaggatcccaaaaa  1397


Query:  961  ggctctccaaggcttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca  1020
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Query: 1081  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt  1140
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Sbjct: 1578  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa  1637


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Query: 1261  tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat  1320
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Query: 1321  tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga  1380
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Query: 1561  agggttaataaaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca  1620
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Query: 1621  gactacaggtgcagaaaacaaagctaaaaaagcttacattgcctctatttggtgccatgaa  1680
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 Score = 222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus

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Sbjct: 2287  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag 2346


Query: 1910  gaaatgaggcctcccacagatctcacacatttttaaagaaacccaaacccatg 1961
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2347  gaaatgaggcctcccacagatctcacacatttttaaagaaacccaaacccatg 2398
```

>gi|7022771|dbj|AK001486.1|AK001486 Homo sapiens cDNA FLJ10624 fis, clone NT2RP2005525, highly
            Mus musculus kanadaptin mRNA
            Length = 2954

 Score = 3470 bits (1750), Expect = 0.0
 Identities = 1757/1760 (99%)
 Strand = Plus / Plus

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438   gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg 497


Query: 61    ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 557


Query: 121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 617


Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 677


Query: 241   ggaggagcagtcgcgcccccacgacagcggtttcttcccctggcggtccagcccgggctcc 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678   ggaggagcagtcgcgcccccacgacagcggtttcttcccctggcggtccagcccgggctcc 737


Query: 301   cccctaccaagagcctccatggggtggccctgccacagcccccctacagcttagagaccct 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738   cccctaccaagagcctccatggggtggccctgccacagcccccctacagcttagagaccct 797
```

```
Query: 361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg 857


Query: 421   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 917


Query: 481   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 918   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta 977


Query: 541   cctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctcg 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 978   cctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctcg 1037


Query: 601   cacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctctt 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038  cacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctctt 1097


Query: 661   tatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacacagtt 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1098  tatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacacagtt 1157


Query: 721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc 780
             |||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||
Sbjct: 1158  gaaggaattgcgcaagcagcagcaaatattgttggagaagaagatgctaagagaagactc 1217


Query: 781   agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1218  agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga 1277


Query: 841   tgagatggggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1278  tgagatggggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 1337


Query: 901   ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1338  ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa 1397


Query: 961   ggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1020
             ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1398  ggttctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1457


Query: 1021  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1458  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca 1517


Query: 1081  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1518  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1577
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Query: 1141  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1578  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa  1637


Query: 1201  aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1638  aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct  1697


Query: 1261  tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1698  tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat  1757


Query: 1321  tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1758  tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga  1817


Query: 1381  actttctgaaatttctgagagattgaaagcctcaagccaagttctatcagagtctccatc  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1818  actttctgaaatttctgagagattgaaagcctcaagccaagttctatcagagtctccatc  1877


Query: 1441  tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1878  tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt  1937


Query: 1501  gtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaacagagacttaa  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1938  gtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaacagagacttaa  1997


Query: 1561  agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1998  agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca  2057


Query: 1621  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2058  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  2117


Query: 1681  aggaggaagcaaattcaaattaaaaactggaacagtagggaagttacccccccaagcgtcc  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2118  aggaggaagcaaattcaaattaaaaactggaacagtagggaagttacccccccaagcgtcc  2177


Query: 1741  agaactccctccaactctaa  1760
             ||||||||||||||||||||
Sbjct: 2178  agaactccctccaactctaa  2197

 Score =  222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus


Query: 1850  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2287  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  2346


Query: 1910  gaaatgaggcctcccacagatctcacacatttttaaagaaacccaaacccatg  1961
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2347 gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg 2398
```

>gi|13636382|ref|XM_002333.3| Homo sapiens hypothetical protein FLJ10624 (FLJ10624), mRNA
           Length = 2949

 Score = 1949 bits (983), Expect = 0.0
 Identities = 990/991 (99%), Gaps = 1/991 (0%)
 Strand = Plus / Plus


```
Query: 770  ggagaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggt 829
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1203 ggagaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggt 1262


Query: 830  agccaagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgat 889
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1263 ag-caagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgat 1321


Query: 890  gctgaagagaaccctattgtcttagagtttcagcaggaaagggaggccttttatataaag 949
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1322 gctgaagagaaccctattgtcttagagtttcagcaggaaagggaggccttttatataaag 1381


Query: 950  gatcccaaaaaggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaa 1009
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1382 gatcccaaaaaggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaa 1441


Query: 1010 tttgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattca 1069
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1442 tttgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattca 1501


Query: 1070 actggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatc 1129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1502 actggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatc 1561


Query: 1130 cagtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagca 1189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1562 cagtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagca 1621


Query: 1190 gtatctcggaaaaggaaagccaagaactgggaagatgaagacttttatgatagtgatgat 1249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1622 gtatctcggaaaaggaaagccaagaactgggaagatgaagacttttatgatagtgatgat 1681


Query: 1250 gacacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaag 1309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1682 gacacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaag 1741


Query: 1310 gctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgat 1369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1742 gctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgat 1801


Query: 1370 gctgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatca 1429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1802 gctgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatca 1861
```

```
Query: 1430  gagtctccatctcaggattcttttagatgcgttcatgtcagaaatgaaatcaggcagtaca  1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1862  gagtctccatctcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtaca  1921


Query: 1490  ttagatggtgtgtcccggaagaaacttcacctgagaacttttgaactgaggaaagaacaa  1549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1922  ttagatggtgtgtcccggaagaaacttcacctgagaacttttgaactgaggaaagaacaa  1981


Query: 1550  cagagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaag  1609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1982  cagagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaag  2041


Query: 1610  actgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctattt  1669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2042  actgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctattt  2101


Query: 1670  ggtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccc  1729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2102  ggtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccc  2161


Query: 1730  cccaagcgtccagaactccctccaactctaa  1760
             |||||||||||||||||||||||||||||||
Sbjct: 2162  cccaagcgtccagaactccctccaactctaa  2192

 Score = 1287 bits (649), Expect = 0.0
 Identities = 693/701 (98%), Gaps = 5/701 (0%)
 Strand = Plus / Plus


Query: 1     gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 437   gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg  496


Query: 61    ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 497   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag  556


Query: 121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 557   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa  616


Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 617   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca  676


Query: 241   ggaggagcagtcgcgcccacgacagcggtttcttcccctggcggtccagcccgggctcc  300
             |||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||
Sbjct: 677   ggaggagcagtcgcgcccccgacagcggtttcttcccctggcggtccag-ccgggctcc  735


Query: 301   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct  360
             |||||||||||||||||||||||||||| | |||||||||||||||||||||||||| |||
Sbjct: 736   cccctaccaagagcctccatggggtgccgctgccacagccccctacagcttagaga-cct  794
```

```
Query: 361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 795   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  854


Query: 421   gaggctgtctggctgcgacgtgtgcctggagcacc-cttcggtgtctcggtaccacgcag  479
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct: 855   gaggctgtctggctgcgacgtgtgcctggagcaccacttcggtgtctcggtaccacgcag  914


Query: 480   tgctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttct  539
             |||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 915   tgctgcagcaca-ggcgtccgg-cctgacggagaatgcgacagcaacgggccgggcttct  972


Query: 540   acctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctc  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 973   acctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctc  1032


Query: 600   gcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctct  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1033  gcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctct  1092


Query: 660   ttatcctgcagggaccagaggaagaccgagaggcagaatcc  700
             |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1093  ttatcctgcagggaccagaggaagaccgagaggcagaatcc  1133
```

 Score = 222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus

```
Query: 1850  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2282  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  2341


Query: 1910  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  1961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2342  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  2393
```

>gi|2661089|gb|AF035526.1|AF035526 Mus musculus kanadaptin mRNA, complete cds
          Length = 2344

 Score = 1340 bits (676), Expect = 0.0
 Identities = 1085/1222 (88%)
 Strand = Plus / Plus


```
Query: 532   gggcttctacctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcat  591
             ||||||| || |||||||||||||||| ||||| ||||| || |||||||||||||||||
Sbjct: 435   gggcttttatctctacgatctgggaagtacccacggcacgttcctcaacaaaactcgcat  494


Query: 592   cccacctcgcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcac  651
             ||||||| ||||| |||||| ||||||||| ||||||||  |  | |||||||||||||||
Sbjct: 495   cccaccccgcacttactgtagagtccacgtcgggcatgtaatgcgctttggaggcagcac  554


Query: 652   ccggctctttatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagt  711
             |||||||||||||||| |||||||||||||||||||||||||||||||| || ||||||||
Sbjct: 555   tcggctctttatccttcagggaccagaggaagaccgagaggcagaatctgaattaacagt  614
```

```
Query: 712   aacacagttgaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctagg   771
             ||||||||||||||||||||||||| ||  |||||||||  |||||  ||||  |||||||||||  ||||
Sbjct: 615   aacacagttgaaggaattgcgtaaacagcagcagatattattggagaagaagatgttagg   674


Query: 772   agaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtag   831
             ||||||||||||||||||||| |||     ||||| ||||| |||||| | |      || |
Sbjct: 675   tgaagactcagatgaagaagaagaagcaaataccactgaagggaagagcagtagaagtgg   734


Query: 832   ccaagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgc   891
             ||||||||||||| |||| |||||| |||||||||||||||||||||||| || |||||||| ||
Sbjct: 735   tcaagatgatgagctgggctgcacgtggggaatgggagaagatgctgtggaggatgaagc   794


Query: 892   tgaagagaaccctattgtcttagagtttcagcaggaaagggaggcctttatataaagga   951
             |||||||||||| |||| ||||||| |||||||||||  ||||| || |||||||||||||||
Sbjct: 795   tgaagagaacccattgccttagattttcagcaggaccgggaagcgttttatataaagga   854


Query: 952   tcccaaaaaggctctccaaggcttttttgaccgagaaggagaagaattagaatatgaatt   1011
             ||| || ||||||||| ||||||||  ||||||||||||||||||||||||| |||||||||||||||
Sbjct: 855   tccaaagaaggctcttcaaggcttctttgaccgagaaggagaagagttagaatatgaatt   914


Query: 1012  tgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattcaac   1071
             |||||| || |||||| ||||||||||||||||||||||||||| |||||||| || ||||||||||
Sbjct: 915   tgatgagcaaggacacagcacttggctctgcagggtgaggttacctgtagatgattcaac   974


Query: 1072  tggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatcca   1131
             |||  |||||  ||||||||||||||||||||||||||||||||||||||||| |||||||||| | ||
Sbjct: 975   tgggaaacagctggtggctgaggccattcactcaggaaagaaaaaggaagcaatggtaca   1034


Query: 1132  gtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagt   1191
             ||||||  ||||||| || ||| | ||||| || |||| ||||| ||||||||||||||||||
Sbjct: 1035  gtgctcgctggaagcctgccgggtccttgatacactgggcttgctacggcaggaagcagt   1094


Query: 1192  atctcggaaaaggaaagccaagaactgggaagatgaagacttttatgatagtgatgatga   1251
             |||||||||||||||||||||||||||||||||||||||||| || |||||||||||||| |||||
Sbjct: 1095  atctcggaaaaggaaagccaagaactgggaagatgaggattttttatgatagtgacgatga   1154


Query: 1252  cacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggc   1311
             |||||  ||  |||  ||||||||||| | |||||||||| ||||| | |||||||||||||
Sbjct: 1155  tacattcctcgatcggactggcctggtagagaagaagcgcctgaaccggatgaagaaggc   1214


Query: 1312  tggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgc   1371
             ||| |||  ||||||||||||||||||| || ||||| ||| ||||||||||||  ||||||||||
Sbjct: 1215  tgggaagcttgatgagaagccagaaacttttgagtcactggttgcaaagttaaatgatgc   1274


Query: 1372  tgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatcaga   1431
             ||||||||||||  | |||||||||||  | | || || ||||||| |||||| ||||||
Sbjct: 1275  cgaaagggaactcgccgaaatttctgaaaggctcaaggcttcaagcaaagttctgtcaga   1334


Query: 1432  gtctccatctcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacatt   1491
             | |  ||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||  |||||
Sbjct: 1335  gccatcatctcaggactctttagatgcattcatgtcagaaatgaaatcaggcagcacatt   1394
```

```
Query: 1492  agatggtgtgtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaaca  1551
             ||||||| |||||||||||||||||||||||||||||||| ||||||||||| || |||||||||||
Sbjct: 1395  agatggggtgtcccggaagaaacttcacctgaggacttttgaactaagaaaagaacaaca  1454


Query: 1552  gagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaagac  1611
             | ||||||||||||||||||||| |||||||||| ||||||||| ||||||||||||||||||
Sbjct: 1455  gcgacttaaagggttaataaaacttgtaaagccggcagagatcccagaactaaaaaagac  1514


Query: 1612  tgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttgg  1671
             ||||    |||||||||| ||||||||||||| |||| || ||| |||||||||| |||||
Sbjct: 1515  tgaacttcagactacaaatgcagaaaacaaaactaagaaacttgcattgcctctctttgg  1574


Query: 1672  tgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttacccccc  1731
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| || ||
Sbjct: 1575  tgccatgaaaggaggaagcaaattcaaattaaaaactgggacagtagggaagttgccacc  1634


Query: 1732  caagcgtccagaactccctcca  1753
             ||||||||||||||||||||||
Sbjct: 1635  caagcgtccagaactccctcca  1656

 Score = 87.7 bits (44), Expect = 3e-14
 Identities = 122/148 (82%)
 Strand = Plus / Plus


Query: 327  gccctgccacagcccccctacagcttagagaccctgaagggcggcactatccttggcaccc  386
            |||| ||||| |||||||||||| | || |||||||||| ||||| |||||||||||||
Sbjct: 230  gcccagccacggcccccctacagtctcgaaaccctgaagggtggcaccatccttggcaccc  289


Query: 387  gtagcttgaaagggacgagttactgccttttcgggaggctgtctggctgcgacgtgtgcc  446
            | | ||||||||| ||||| | |||| |||||||||| || || | || ||| | || |
Sbjct: 290  gcaccttgaaagacacgagctgctgctttttcgggagacttgctagttgtgacatatgtc  349


Query: 447  tggagcacccttcggtgtctcggtacca  474
            ||||||| ||||| ||||||||||||||
Sbjct: 350  tggagcatccttccgtgtctcggtacca  377
```

>gi|1029496|emb|Z58265.1|HS33F3R H.sapiens CpG island DNA genomic Mse1 fragment, clone 33f3, r
            read cpg33f3.rt1f
            Length = 290

```
 Score =  428 bits (216), Expect = e-117
 Identities = 226/230 (98%)
 Strand = Plus / Minus


Query: 442  gtgcctggagcacccttcggtgtctcggtaccacgcagtgctgcagcacagggcgtccgg  501
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 290  gtgcctggagcacccttcggtgtctcggtaccacgcagtgctgcagcacagggcgtctgg  231


Query: 502  ccctgacggagaatgcgacagcaacgggccgggcttctacctctacgatctgggaagcac  561
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 230  ccctgacggagaatgcgacagcaacgggccgggcttctacctctacgatctgggaagcac  171


Query: 562  ccatggcacttttctcaacaaaactcgcatcccacctcgcacctactgtcgagtccacgt  621
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
```

```
Sbjct:  170  ccatggcacttttctcaacaaaactcgcatcccacctcgcacctactgtcgagnccacgt  111


Query:  622  tgggcatgttgttcgctttggaggcagcacccggctctttatcctgcagg  671
             |||||||||||||||||||||||||| ||||||||| ||||||||||||||
Sbjct:  110  tgggcatgttgttcgctttggagacagcacccgnctctttatcctgcagg  61

>gi|11182219|emb|AL357559.16|AL357559 Human DNA sequence from clone RP11-393M18 on chromosome
             sequence [Homo sapiens]
          Length = 190912

 Score =  141 bits (71), Expect = 2e-30
 Identities = 144/167 (86%), Gaps = 1/167 (0%)
 Strand = Plus / Plus


Query:  1551    agagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaaga  1610
               |||||||||||||| || ||||||||||||||||||||||||   ||||||||| | ||
Sbjct:  189905  agagacttaaaggattgataaaaattgtaaagccagcagagacctcagaactaaacatga  189964


Query:  1611    ctgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttg  1670
                |||| | |||||| || |||| |   | ||||||| ||||||||| |||| |||| || |
Sbjct:  189965  ttgaaaattagactaaagatgcacacga-aaagctacaaagcttatattgactctcttgg  190023


Query:  1671    gtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagta  1717
               ||||||| ||||||||||||||||| |||||||||||||||||||||
Sbjct:  190024  gtgccataaaaggaggaagcaaattgaaattaaaaactggaacagta  190070

 Score = 91.7 bits (46), Expect = 2e-15
 Identities = 64/70 (91%)
 Strand = Plus / Plus


Query:  1307    aaggctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaat  1366
               |||||||| |||||||||||||||| |||||||||||| || | |||||||||| ||||||
Sbjct:  189691  aaggctgggaagattgatgagaaggcagagacctttgcattactggttgcaaagttaaat  189750


Query:  1367    gatgctgaaa  1376
               ||||||||||
Sbjct:  189751  gatgctgaaa  189760

 Score = 87.7 bits (44), Expect = 3e-14
 Identities = 65/72 (90%)
 Strand = Plus / Plus


Query:  1407    aagcctcaagccaagttctatcagagtctccatctcaggattctttagatgcgttcatgt  1466
               |||||||||||| |||||||||||| || | ||||||||| |||||||||| ||||||||
Sbjct:  189765  aagcctcaagcaaagttctatcagaatcacaatctcaggcttctttagatgtgttcatgt  189824


Query:  1467    cagaaatgaaat  1478
               ||||| ||||||
Sbjct:  189825  cagaagtgaaat  189836

 Score = 73.9 bits (37), Expect = 5e-10
 Identities = 40/41 (97%)
 Strand = Plus / Plus


Query:  1213    gaactgggaagatgaagacttttatgatagtgatgatgaca  1253
               ||||||||||||||||||||||||||||| |||||||||||
```

```
Sbjct: 189600 gaactgggaagatgaagactttatgagagtgatgatgaca 189640

 Score = 56.0 bits (28), Expect = 1e-04
 Identities = 28/28 (100%)
 Strand = Plus / Plus


Query: 996    aattagaatatgaatttgatgaacaggg 1023
              ||||||||||||||||||||||||||||
Sbjct: 189384 aattagaatatgaatttgatgaacaggg 189411

 Score = 44.1 bits (22), Expect = 0.44
 Identities = 58/70 (82%)
 Strand = Plus / Plus


Query: 658    ctttatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacaca 717
              |||| |||||||| ||||||||| |||||| || || | ||||||| ||| |||||||  ||
Sbjct: 189057 ctttgtcctgcaaggaccagaagaagactgaaagactgaatccaagtgaacagtagtgca 189116


Query: 718    gttgaaggaa 727
              ||||||||||
Sbjct: 189117 gttgaaggaa 189126

 Score = 40.2 bits (20), Expect = 6.9
 Identities = 60/72 (83%), Gaps = 1/72 (1%)
 Strand = Plus / Plus


Query: 1064   gattcaactggaaaacaactggtggctgaggccattcactcaggaaagaaaaaa-gaagc 1122
              |||||| |||||||||||||     ||||||| |||||| |||| |||| ||||||||| ||| |
Sbjct: 189447 gattcatctggaaaacaacgccaggctgaagccatgcacttaggagagaaaaaaggaaac 189506


Query: 1123   aatgatccagtg 1134
              || |||||||||
Sbjct: 189507 aaagatccagtg 189518

>gi|11181843|gb|AC017028.11|AC017028 Homo sapiens BAC clone RP11-275G7 from 2, complete sequen
          Length = 201971

 Score = 48.1 bits (24), Expect = 0.028
 Identities = 27/28 (96%)
 Strand = Plus / Minus


Query: 1968   tctttcttctccttcctgtgttgttcag 1995
              |||||||||| |||||||||||||||||
Sbjct: 172682 tctttcttcttcttcctgtgttgttcag 172655

>gi|14010785|gb|AC069543.4|AC069543 Homo sapiens chromosome 10 clone RP11-393H5, complete sequ
          Length = 179787

 Score = 46.1 bits (23), Expect = 0.11
 Identities = 23/23 (100%)
 Strand = Plus / Plus


Query: 984    gagaaggagaagaattagaatat 1006
              |||||||||||||||||||||||
Sbjct: 127574 gagaaggagaagaattagaatat 127596

>gi|10443437|emb|AL356421.10|AL356421 Human DNA sequence from clone RP11-550C4 on chromosome 6
          sequence [Homo sapiens]
```

Length = 170532

Score = 46.1 bits (23), Expect = 0.11
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1680   aaggaggaagcaaattcaaatta 1702
              |||||||||||||||||||||||
Sbjct: 92560 aaggaggaagcaaattcaaatta 92538

  Database: nt
    Posted date: May 11, 2001 4:10 AM
  Number of letters in database: -1,072,656,299
  Number of sequences in database: 858,416

Lambda   K   H
    1.37   0.711   1.31

Gapped
Lambda   K   H
    1.37   0.711   1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6729269
Number of Sequences: 858416
Number of extensions: 6729269
Number of successful extensions: 48683
Number of sequences better than 10.0: 87
length of query: 2644
length of database: 3,222,310,993
effective HSP length: 22
effective length of query: 2622
effective length of database: 3,203,425,841
effective search space: 8399382555102
effective search space used: 8399382555102
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 20 (40.2 bits)